

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 17, 2002, 01:23:59 ; Search time 86.97 Seconds
(without alignments)
2601.489 Million cell updates/sec

Title: US-09-439-311-1

Perfect score: 999

Sequence: 1 attacacacaaatgttgcgc.....ttaaaatgatgttagagat 999

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 11328999 residues

Total number of hits satisfying chosen parameters: 515962

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	26.8	2.7	30	4	US-09-358-972-102
C 2	26.8	2.7	30	4	US-09-358-972-103
C 3	26.8	2.7	30	4	US-09-406-147-32
C 4	26.8	2.7	30	4	US-09-406-147-34
C 5	20.8	2.1	24	1	US-08-587-209-6
C 6	20.8	2.1	24	1	US-08-689-236-6
C 7	20.8	2.1	24	1	US-08-689-236-6
C 8	20.8	2.1	24	1	US-08-692-725-6
C 9	20.8	2.1	24	2	US-08-692-725-6
C 10	20.8	2.1	58	2	US-08-431-527A-7
C 11	20.8	2.1	58	2	US-09-214-278-30
C 12	20.6	2.1	52	3	US-08-886-967-3
C 13	20.6	2.1	52	3	US-09-306-949-3
C 14	20	2.0	39	3	US-08-874-825-118
C 15	20	2.0	50	3	US-08-450-9058-7
C 16	20	2.0	50	3	US-07-982-759F-7
C 17	20	2.0	57	1	US-08-141-892A-4
C 18	20	2.0	57	1	US-08-583-447A-4
C 19	20	2.0	57	2	US-08-467-920-4
C 20	20	2.0	57	3	US-08-635-930-4
C 21	20	2.0	57	3	US-09-193-997-4
C 22	20	2.0	57	3	US-09-138-237A-4
C 23	20	2.0	60	1	US-08-478-370-4
C 24	19.6	2.0	43	1	US-07-959-946-12
C 25	19.6	2.0	43	1	US-08-333-577-12
C 26	19.6	2.0	43	5	PCT-US92-08634-12
C 27	19.6	2.0	58	1	US-08-105-483-174

C 28	19.6	2.0	58	1	US-08-709-209-174
C 29	19.6	2.0	58	1	US-08-303-275-62
C 30	19.6	2.0	58	1	US-08-458-101-174
C 31	19.6	2.0	60	1	US-07-670-236-19
C 32	19.6	2.0	60	1	US-08-093-781-20
C 33	19.6	2.0	60	3	US-08-963-602-2
C 34	19.4	1.9	37	2	US-08-403-853-8
C 35	19.4	1.9	60	1	US-08-487-890A-127
C 36	19.4	1.9	60	2	US-08-478-435-127
C 37	19.4	1.9	60	2	US-08-337-483-127
C 38	19.4	1.9	60	2	US-08-478-373-127
C 39	19.4	1.9	60	3	US-08-474-671-127
C 40	19.4	1.9	60	3	US-08-483-577A-127
C 41	19.4	1.9	60	4	US-08-897-438-127
C 42	19.2	1.9	58	2	US-08-431-527A-6
C 43	19.2	1.9	60	1	US-07-609-716-72
C 44	19.2	1.9	60	3	US-08-475-411A-72
C 45	19.2	1.9	60	4	US-08-478-029A-72

ALIGNMENTS

RESULT 1
US-09-358-972-102/c
; Sequence 102, Application US/09358972
; Patent No. 6235480
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W.
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09/358.972
; CURRENT FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 102
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: probe to Campylobacter jejuni
US-09-358-972-102

Query Match 2.7%; Score 36.8; DB 4; Length 30;
Best Local Similarity 93.3%; Pred. No. 82;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 289 caagatggtcgaagcttaaaacagaact 318
||||| ||||| ||||| ||||| |||||
DB 30 CAAGATGCACAAAGTTTAAACAAAGAACT 1

RESULT 2
US-09-358-972-103
; Sequence 103, Application US/09358972
; Patent No. 6235480
; GENERAL INFORMATION:

OY 91 ggtcttagaataactccgcagca 114
 |||||
 Db 24 GGTCTTAGAATTAACTCAGCAGCA 1

RESULT 13

AAV25942/C
 ID AAV25942 standard; DNA: 24 BP.

XX AC AAV25942;
 XX
 XX 15-JUL-1998 (first entry)
 XX
 XX Oligonucleotide PCR primer CFOAR gene.

XX Sequence-specific; probe: enterohaemorrhagic; Escherichia coli;
 KW Salmonella; Campylobacter; Shigella; Yersinia; beta-globin;
 KW gastroenteritis; PCR primer; ss.

XX Synthetic.
 OS Campylobacter sp.

XX US5753444-A.
 PN 19-MAY-1998.

XX 07-AUG-1996; 96US-0689235.

XX 16-JAN-1996; 96US-0587209.

PR 07-AUG-1996; 96US-0689235.

XX (GULL-) GULL LAB INC.

XX Coombs J, Glass MJ, Malmstrom SL, Wu L;
 PI WPI; 1998-311393/27.

XX Distinguishing between similar nucleic acid samples - using
 PT sequence-specific probes e.g. between enterohaemorrhagic and normal
 PT Escherichia coli

XX Example 3: Column 17; 21pp; English.

CC The present sequence represents a PCR primer used in an example of the
 CC present invention. The present invention describes a method for
 CC detecting mismatches between first and second nucleic acid sequences
 CC having at least one base difference. The method comprises: (a) obtaining
 CC at least one labelled probe consisting of an oligonucleotide sequence
 CC spanning the location of at least one base difference between the first
 CC and second sequences, where the oligonucleotide sequence contains at
 CC least one neutral base molecule in a position other than the position of
 CC the base difference(s) but is otherwise exactly complementary to the
 CC first sequence, so that the probe hybridises more weakly with the second
 CC sequence than with the first sequence; (b) mixing the probe(s) with the
 CC first and second sequences under hybridisation conditions; (c)
 CC dissociating any probe/second sequence hybrids; and (d) detecting
 CC probe/first sequence hybrids. The method can be used to distinguish
 CC between similar DNA/RNA sequences in a sample, especially to distinguish
 CC enterohaemorrhagic E. coli O157:H7 from other E. coli strains e.g. in
 CC stool samples from people suffering from gastroenteritis, caused
 CC specifically by enterohaemorrhagic E. coli. Use of the method shortens
 CC the time between sample preparation to obtaining results, than has been
 CC possible with previous similar procedures.

XX Sequence 24 BP; 6 A; 5 C; 5 G; 8 T; 0 other;

Query Match

Best Local Similarity 2.1%; Score 20.8; DB 19; Length 24;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 91 ggtcttagaataactccgcagca 114

|||||
 Db 24 GGTCTTAGAATTAACTCAGCAGCA 1

RESULT 14

AAV20847/C
 ID AAV20847 standard; DNA: 24 BP.

XX AC AAV20847;
 XX

XX 01-JUL-1998 (first entry)
 XX

XX Campylobacter CFOAR gene PCR primer.

XX Escherichia coli strain O157:H7; detection; microorganism; infection;
 KW enterohaemorrhagic; PCR primer; ss.

XX Synthetic.

OS Campylobacter sp.

XX US5738995-A.

PN 14-APR-1998.

XX 07-AUG-1996; 96US-0689236.

XX 16-JAN-1996; 96US-0587209.

PR 07-AUG-1996; 96US-0689236.

XX (GULL-) GULL LAB INC.

XX Coombs J, Glass MJ, Malmstrom SL, Wu L;
 PI WPI; 1998-260031/23.

XX Probes for detecting Escherichia coli strain O157:H7 - useful for
 PT diagnosis of enterohaemorrhagic Escherichia coli infection(s)

XX Example 3: Column 17; 21pp; English.

CC The present sequence represents a PCR primer used in an example of the
 CC present invention. The present invention describes probes used in the
 CC detection of Escherichia coli strain O157:H7 in a sample. The method of
 CC detection comprises: (a) obtaining at least 1 probe specifically given
 CC in the specification, labelled with a label that permits probe detection
 CC when hybridised to a complementary nucleic acid sequence which is
 CC specific for a nucleic acid sequence of the microorganism; (b)
 CC hybridising the probes and the sample, and (c) detecting hybrids
 CC comprising the probes and the nucleic acid sequences. The method and
 CC probes may be used for diagnosis of enterohaemorrhagic E. coli
 CC infections. The methods and the materials permit the detection and
 CC discrimination of multiple analytes.

XX Sequence 24 BP; 6 A; 5 C; 5 G; 8 T; 0 other;

Query Match

Best Local Similarity 2.1%; Score 20.8; DB 19; Length 24;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 91 ggtcttagaataactccgcagca 114
 |||||

Db 24 GGTCTTAGAATTAACTCAGCAGCA 1

RESULT 15

AAV16711
 ID AAV16711 standard; DNA: 44 BP.

XX AC AAV16711;
 XX

XX 09-MAR-2001 (first entry)
 XX

